

SEQUENCE LISTING.txt
SEQUENCE LISTING

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<120> Mutant Bacillus

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<150> JP 2004-062852

<151> 2004.03.05

<160> 28

<170> PatentIn Ver. 3.1

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<212> PRT

<213> Bacillus subtilis

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Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu
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SEQUENCE LISTING.txt

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SEQUENCE LISTING.txt

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Pro Arg Asp Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile
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Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu
165 170 175

Glu Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met
180 185 190

Leu Arg Asp Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser
195 200 205

Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp
210 215 220

Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala
225 230 235 240

Ala Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly
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SEQUENCE LISTING.txt

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 Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro
 545 550 555 560

SEQUENCE LISTING.txt

Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu
565 570 575

Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn
580 585 590

Ala Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn
595 600 605

Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg
610 615 620

Gly Glu Asn Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg
625 630 635 640

Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr
645 650 655

Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp
660 665 670

Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val
675 680 685

Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu
690 695 700

Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly
705 710 715 720

Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu
725 730 735

Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val
740 745 750

Asp Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu
755 760 765

Lys Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys
770 775 780

Ala Ile Lys Asn Glu Ala Thr Lys Lys
785 790

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SEQUENCE LISTING.txt

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<221> sig_peptide

<222> (610)..(696)

<223>

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cctgatttta tttttttgaa tttttttgag aactaaagat tgaaatagaa gtagaagaca 180

acggacataa gaaaattgta ttagttttta ttatagaaaa cgcttttcta taattattta 240

tacctagaac gaaaatactg tttcgaaagc ggtttactat aaaaccttat attccggctc 300

tttttttaaa caggggggtga aaattcactc tagtattcta atttcaacat gctataataa 360

atttgtaaga cgcaatatac atcttttttt tatgatattt gtaagcgggtt aaccttgtgc 420

tatatgccga tttaggaagg gggtagattg agtcaagtag tcataattta gataacttat 480

aagttgttga gaagcaggag agaatctggg ttactcacia gtttttttaa acattatcga 540

aagcactttc ggttatgctt atgaatttag ctatttgatt caattacttt aataatttta 600

ggaggtaat atg atg tta aga aag aaa aca aag cag ttg att tct tcc att 651
Met Met Leu Arg Lys Lys Thr Lys Gln Leu Ile Ser Ser Ile
-25 -20ctt att tta gtt tta ctt cta tct tta ttt ccg aca gct ctt gca gca 699
Leu Ile Leu Val Leu Leu Leu Ser Leu Phe Pro Thr Ala Leu Ala Ala
-15 -10 -5 -1 1gaa gga aac act cgt gaa gac aat ttt aaa cat tta tta ggt aat gac 747
Glu Gly Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp
5 10 15aat gtt aaa cgc cct tct gag gct ggc gca tta caa tta caa gaa gtc 795
Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val
20 25 30gat gga caa atg aca tta gta gat caa cat gga gaa aaa att caa tta 843
Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu
35 40 45cgt gga atg agt aca cac gga tta caa tgg ttt cct gag atc ttg aat 891
Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn
50 55 60 65gat aac gca tac aaa gct ctt gct aac gat tgg gaa tca aat atg att 939
Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met Ile
70 75 80cgt cta gct atg tat gtc ggt gaa aat ggc tat gct tca aat cca gag 987
Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro Glu
85 90 95tta att aaa agc aga gtc att aaa gga ata gat ctt gct att gaa aat 1035
Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu Asn
100 105 110

SEQUENCE LISTING.txt

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aga Arg 130	gat Asp	ccc Pro	gtt Val	tac Tyr	gct Ala 135	gga Gly	gca Ala	gaa Glu	gat Asp	ttc Phe 140	ttt Phe	aga Arg	gat Asp	att Ile	gca Ala 145	1131
gca Ala	tta Leu	tat Tyr	cct Pro	aac Asn 150	aat Asn	cca Pro	cac His	att Ile	att Ile 155	tat Tyr	gag Glu	tta Leu	gcg Ala	aat Asn 160	gag Glu	1179
cca Pro	agt Ser	agt Ser	aac Asn 165	aat Asn	aat Asn	ggt Gly	gga Gly	gct Ala 170	ggg Gly	att Ile	cca Pro	aat Asn	aat Asn 175	gaa Glu	gaa Glu	1227
ggt Gly	tgg Trp	aat Asn 180	gcg Ala	gta Val	aaa Lys	gaa Glu	tac Tyr 185	gct Ala	gat Asp	cca Pro	att Ile	gta Val 190	gaa Glu	atg Met	tta Leu	1275
cgt Arg	gat Asp 195	agc Ser	ggg Gly	aac Asn	gca Ala	gat Asp 200	gac Asp	aat Asn	att Ile	atc Ile	att Ile 205	gtg Val	ggt Gly	agt Ser	cca Pro	1323
aac Asn 210	tgg Trp	agt Ser	cag Gln	cgt Arg	cct Pro 215	gac Asp	tta Leu	gca Ala	gct Ala	gat Asp 220	aat Asn	cca Pro	att Ile	gat Asp	gat Asp 225	1371
cac His	cat His	aca Thr	atg Met	tat Tyr 230	act Thr	gtt Val	cac His	ttc Phe	tac Tyr 235	act Thr	ggt Gly	tca Ser	cat His	gct Ala 240	gct Ala	1419
tca Ser	act Thr	gaa Glu	agc Ser 245	tat Tyr	ccg Pro	cct Pro	gaa Glu	act Thr 250	cct Pro	aac Asn	tct Ser	gaa Glu	aga Arg 255	gga Gly	aac Asn	1467
gta Val	atg Met	agt Ser 260	aac Asn	act Thr	cgt Arg	tat Tyr	gcg Ala 265	tta Leu	gaa Glu	aac Asn	gga Gly	gta Val 270	gca Ala	gta Val	ttt Phe	1515
gca Ala 275	aca Thr	gag Glu	tgg Trp	gga Gly	act Thr	agc Ser 280	caa Gln	gca Ala	aat Asn	gga Gly	gat Asp 285	ggt Gly	ggt Gly	cct Pro	tac Tyr	1563
ttt Phe 290	gat Asp	gaa Glu	gca Ala	gat Asp	gta Val 295	tgg Trp	att Ile	gag Glu	ttt Phe	tta Leu 300	aat Asn	gaa Glu	aac Asn	aac Asn	att Ile 305	1611
agc Ser	tgg Trp	gct Ala	aac Asn	tgg Trp 310	tct Ser	tta Leu	acg Thr	aat Asn	aaa Lys 315	aat Asn	gaa Glu	gta Val	tct Ser	ggt Gly 320	gca Ala	1659
ttt Phe	aca Thr	cca Pro	ttc Phe 325	gag Glu	tta Leu	ggt Gly	aag Lys	tct Ser 330	aac Asn	gca Ala	aca Thr	agt Ser	ctt Leu 335	gac Asp	cca Pro	1707
ggg Gly	cca Pro	gac Asp 340	caa Gln	gta Val	tgg Trp	gta Val	cca Pro 345	gaa Glu	gag Glu	tta Leu	agt Ser	ctt Leu 350	tct Ser	gga Gly	gaa Glu	1755
tat Tyr	gta Val 355	cgt Arg	gct Ala	cgt Arg	att Ile	aaa Lys 360	ggt Gly	gtg Val	aac Asn	tat Tyr	gag Glu 365	cca Pro	atc Ile	gac Asp	cgt Arg	1803
aca Thr 370	aaa Lys	tac Tyr	acg Thr	aaa Lys	gta Val 375	ctt Leu	tgg Trp	gac Asp	ttt Phe	aat Asn 380	gat Asp	gga Gly	acg Thr	aag Lys	caa Gln 385	1851

SEQUENCE LISTING.txt

gga ttt gga gtg aat gga gat tct cca gtt gaa gat gta gtt att gag Gly Phe Gly Val Asn Gly Asp Ser Pro Val Glu Asp Val Val Ile Glu 390 395 400	1899
aat gaa gcg ggc gct tta aaa ctt tca gga tta gat gca agt aat gat Asn Glu Ala Gly Ala Leu Lys Leu Ser Gly Leu Asp Ala Ser Asn Asp 405 410 415	1947
gtt tct gaa ggt aat tac tgg gct aat gct cgt ctt tct gcc gac ggt Val Ser Glu Gly Asn Tyr Trp Ala Asn Ala Arg Leu Ser Ala Asp Gly 420 425 430	1995
tgg gga aaa agt gtt gat att tta ggt gct gaa aaa ctt act atg gat Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met Asp 435 440 445	2043
gtg att gtt gat gag ccg acc acg gta tca att gct gca att cca caa Val Ile Val Asp Glu Pro Thr Thr Val Ser Ile Ala Ala Ile Pro Gln 450 455 460 465	2091
ggg cca tca gcc aat tgg gtt aat cca aat cgt gca att aag gtt gag Gly Pro Ser Ala Asn Trp Val Asn Pro Asn Arg Ala Ile Lys Val Glu 470 475 480	2139
cca act aat ttc gta ccg tta gga gat aag ttt aaa gcg gaa tta act Pro Thr Asn Phe Val Pro Leu Gly Asp Lys Phe Lys Ala Glu Leu Thr 485 490 495	2187
ata act tca gct gac tct cca tcg tta gaa gct att gcg atg cat gct Ile Thr Ser Ala Asp Ser Pro Ser Leu Glu Ala Ile Ala Met His Ala 500 505 510	2235
gaa aat aac aac atc aac aac atc att ctt ttt gta gga act gaa ggt Glu Asn Asn Asn Ile Asn Asn Ile Ile Leu Phe Val Gly Thr Glu Gly 515 520 525	2283
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tta tca tgg gaa ttt gga tac cca gaa gta aaa cct agt gat aac tgg Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn Trp 595 600 605	2523
gca aca gct cca cgt tta gat ttc tgg aaa tct gac ttg gtt cgc ggt Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg Gly 610 615 620 625	2571
gaa aat gat tat gta act ttt gat ttc tat cta gat cca gtt cgt gca Glu Asn Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala 630 635 640	2619
aca gaa ggc gca atg aat atc aat tta gta ttc cag cca cct act aac Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn 645 650 655	2667

SEQUENCE LISTING.txt

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tta gag gaa gcg aat caa gta aat ggt tta tat cac tat gaa gtg aaa Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys 675 680 685	2763
att aac gta aga gat att aca aac att caa gat gac acg tta cta cgt Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg 690 695 700 705	2811
aac atg atg atc att ttt gca gat gta gaa agt gac ttt gca ggg aga Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg 710 715 720	2859
gtc ttt gta gat aat gtt cgt ttt gag ggg gct gct act act gag ccg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro 725 730 735	2907
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atc aaa aat gag gct acg aaa aaa taatctaata aactagttat agggttatct Ile Lys Asn Glu Ala Thr Lys Lys 790	3105
aaaggctctga tgcagatctt ttagataacc tttttttgca taactggaca tagaatgggtt	3165
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ttaataatgt cttgtgatag aatgatgaag taatttaaga gggggaaaacg aagtgaaaac	3285
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<220>
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<400> 8
 atggctgata aacaaacca 20

<210> 9
 <211> 20
 <212> DNA
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<220>
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SEQUENCE LISTING.txt

<400> 9
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<210> 10
<211> 21
<212> DNA
<213> artificial sequence

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<400> 10
acagcctttc ttcctcattc t 21

<210> 11
<211> 42
<212> DNA
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<220>
<223> oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of the upstream region of sigH in Bacillus subtilis and its 5'-portion designed from nucleotide sequence of sigA in Bacillus subtilis

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cgtgggtttg tttatcagcc attccgatcc ccccggcgca cg 42

<210> 12
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<210> 13
<211> 42
<212> DNA
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<220>
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<212> DNA
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SEQUENCE LISTING.txt

<400> 14
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<210> 15
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<220>
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<210> 16
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<220>
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<400> 16
atagctgata aacaaaccca 20

<210> 17
<211> 42
<212> DNA
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<220>
<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of the upstream region of sigF in *Bacillus subtilis* and its 5'-portion designed from nucleotide sequence of sigA in *Bacillus subtilis*; the sequence containing a nucleotide substitution for destroying the initiation codon of sigA

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SEQUENCE LISTING.txt

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aaatgacatc atataaaciaa atttgtctac caatcactat ttaaagctgt ttatgatata	180
tgtaagcggt atcattaaaa ggagggtatgt g atg aga aga tgg gta gta gca	232
Met Arg Arg Trp Val Val Ala	
-20 -15	
atg ttg gca gtg tta ttt tta ttt cct tcg gta gta gtt gca gat gga	280
Met Leu Ala Val Leu Phe Leu Phe Pro Ser Val Val Val Ala Asp Gly	
-10 -5 -1 1	
ttg aac ggt acg atg atg cag tat tat gag tgg cat ttg gaa aac gac	328
Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu Asn Asp	
5 10 15	
ggg cag cat tgg aat cgg ttg cac gat gat gcc gca gct ttg agt gat	376
Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Leu Ser Asp	
20 25 30	
gct ggt att aca gct att tgg att ccg cca gcc tac aaa ggt aat agt	424
Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly Asn Ser	
35 40 45 50	
cag gcg gat gtt ggg tac ggt gca tac gat ctt tat gat tta gga gag	472
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu	
55 60 65	
ttc aat caa aag ggt act gtt cga acg aaa tac gga act aag gca cag	520
Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ala Gln	
70 75 80	
ctt gaa cga gct att ggg tcc ctt aaa tct aat gat atc aat gta tac	568
Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn Val Tyr	
85 90 95	
gga gat gtc gtg atg aat cat aaa atg gga gct gat ttt acg gag gca	616
Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr Glu Ala	
100 105 110	
gtg caa gct gtt caa gta aat cca acg aat cgt tgg cag gat att tca	664
Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp Ile Ser	
115 120 125 130	
ggt gcc tac acg att gat gcg tgg acg ggt ttc gac ttt tca ggg cgt	712
Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser Gly Arg	
135 140 145	
aac aac gcc tat tca gat ttt aag tgg aga tgg ttc cat ttt aat ggt	760
Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe Asn Gly	
150 155 160	
gtt gac tgg gat cag cgc tat caa gaa aat cat att ttc cgc ttt gca	808
Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg Phe Ala	
165 170 175	
aat acg aac tgg aac tgg cga gtg gat gaa gag aac ggt aat tat gat	856
Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn Tyr Asp	
180 185 190	
tac ctg tta gga tcg aat atc gac ttt agt cat cca gaa gta caa gat	904
Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val Gln Asp	
195 200 205 210	

SEQUENCE LISTING.txt

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Glu	Leu	Lys	Asp	Trp	Gly	Ser	Trp	Phe	Thr	Asp	Glu	Leu	Asp	Leu	Asp	
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ggt	tat	cgt	tta	gat	gct	att	aaa	cat	att	cca	ttc	tgg	tat	aca	tct	1000
Gly	Tyr	Arg	Leu	Asp	Ala	Ile	Lys	His	Ile	Pro	Phe	Trp	Tyr	Thr	Ser	
			230					235					240			
gat	tgg	ggt	cgg	cat	cag	cgc	aac	gaa	gca	gat	caa	gat	tta	ttt	gtc	1048
Asp	Trp	Val	Arg	His	Gln	Arg	Asn	Glu	Ala	Asp	Gln	Asp	Leu	Phe	Val	
		245					250					255				
gta	ggg	gaa	tat	tgg	aag	gat	gac	gta	ggt	gct	ctc	gaa	ttt	tat	tta	1096
Val	Gly	Glu	Tyr	Trp	Lys	Asp	Asp	Val	Gly	Ala	Leu	Glu	Phe	Tyr	Leu	
	260					265					270					
gat	gaa	atg	aat	tgg	gag	atg	tct	cta	ttc	gat	ggt	cca	ctt	aat	tat	1144
Asp	Glu	Met	Asn	Trp	Glu	Met	Ser	Leu	Phe	Asp	Val	Pro	Leu	Asn	Tyr	
					280					285					290	
aat	ttt	tac	cgg	gct	tca	caa	caa	ggt	gga	agc	tat	gat	atg	cgt	aat	1192
Asn	Phe	Tyr	Arg	Ala	Ser	Gln	Gln	Gly	Gly	Ser	Tyr	Asp	Met	Arg	Asn	
				295					300					305		
att	tta	cga	gga	tct	tta	gta	gaa	gcg	cat	ccg	atg	cat	gca	gtt	acg	1240
Ile	Leu	Arg	Gly	Ser	Leu	Val	Glu	Ala	His	Pro	Met	His	Ala	Val	Thr	
			310					315					320			
ttt	ggt	gat	aat	cat	gat	act	cag	cca	ggg	gag	tca	tta	gag	tca	tgg	1288
Phe	Val	Asp	Asn	His	Asp	Thr	Gln	Pro	Gly	Glu	Ser	Leu	Glu	Ser	Trp	
		325					330					335				
gtt	gct	gat	tgg	ttt	aag	cca	ctt	gct	tat	gcg	aca	att	ttg	acg	cgt	1336
Val	Ala	Asp	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Thr	Ile	Leu	Thr	Arg	
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gaa	ggt	ggt	tat	cca	aat	gta	ttt	tac	ggt	gat	tac	tat	ggg	att	cct	1384
Glu	Gly	Gly	Tyr	Pro	Asn	Val	Phe	Tyr	Gly	Asp	Tyr	Tyr	Gly	Ile	Pro	
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aac	gat	aac	att	tca	gct	aaa	aaa	gat	atg	att	gat	gag	ctg	ctt	gat	1432
Asn	Asp	Asn	Ile	Ser	Ala	Lys	Lys	Asp	Met	Ile	Asp	Glu	Leu	Leu	Asp	
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gca	cgt	caa	aat	tac	gca	tat	ggc	acg	cag	cat	gac	tat	ttt	gat	cat	1480
Ala	Arg	Gln	Asn	Tyr	Ala	Tyr	Gly	Thr	Gln	His	Asp	Tyr	Phe	Asp	His	
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tgg	gat	ggt	gta	gga	tgg	act	agg	gaa	gga	tct	tcc	tcc	aga	cct	aat	1528
Trp	Asp	Val	Val	Gly	Trp	Thr	Arg	Glu	Gly	Ser	Ser	Ser	Arg	Pro	Asn	
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tca	ggc	ctt	gcg	act	att	atg	tcg	aat	gga	cct	ggt	ggt	tcc	aag	tgg	1576
Ser	Gly	Leu	Ala	Thr	Ile	Met	Ser	Asn	Gly	Pro	Gly	Gly	Ser	Lys	Trp	
			420			425					430					
atg	tat	gta	gga	cgt	cag	aat	gca	gga	caa	aca	tgg	aca	gat	tta	act	1624
Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Gln	Thr	Trp	Thr	Asp	Leu	Thr	
					440					445					450	
ggt	aat	aac	gga	gcg	tcc	gtt	aca	att	aat	ggc	gat	gga	tgg	ggc	gaa	1672
Gly	Asn	Asn	Gly	Ala	Ser	Val	Thr	Ile	Asn	Gly	Asp	Gly	Trp	Gly	Glu	
				455					460					465		
ttc	ttt	acg	aat	gga	gga	tct	gta	tcc	gtg	tac	gtg	aac	caa	taacaaaa	1723	
Phe	Phe	Thr	Asn	Gly	Gly	Ser	Val	Ser	Val	Tyr	Val	Asn	Gln			
			470					475					480			

SEQUENCE LISTING.txt

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tctacgactt tg 1795

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<212> PRT
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Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu
20 25 30

Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
50 55 60

Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
85 90 95

Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr
100 105 110

Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp
115 120 125

Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
130 135 140

Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
145 150 155 160

Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg
165 170 175

Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
180 185 190

Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
195 200 205

Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
210 215 220

SEQUENCE LISTING.txt

Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
 225 230 235 240
 Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu
 245 250 255
 Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
 260 265 270
 Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
 275 280 285
 Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met
 290 295 300
 Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala
 305 310 315 320
 Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu
 325 330 335
 Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
 340 345 350
 Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
 355 360 365
 Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
 370 375 380
 Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
 385 390 395 400
 Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg
 405 410 415
 Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
 420 425 430
 Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp
 435 440 445
 Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
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 Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
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 <211> 1441
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SEQUENCE LISTING.txt

<213> Bacillus clausii KSM-K16

<220>

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<223>

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acttaatggt aataattggt tccaatagg caaatctttc taactttgat acgtttaaac	120
taccagcttg gacgagttgg gataaaagtg aggagggaac cga atg aag aaa ccg	175
	Met Lys Lys Pro
	1
ttg ggg aaa att gtc gca agc acc gca cta ctc att tct gtt gct ttt	223
Leu Gly Lys Ile Val Ala Ser Thr Ala Leu Leu Ile Ser Val Ala Phe	20
5	
agt tca tcg atc gca tcg gct gct gag gaa gca aaa gaa aaa tat tta	271
Ser Ser Ser Ile Ala Ser Ala Ala Glu Glu Ala Lys Glu Lys Tyr Leu	35
25	
att ggc ttt aat gag cag gaa gca gtt agt gag ttt gta gag caa ata	319
Ile Gly Phe Asn Glu Gln Glu Ala Val Ser Glu Phe Val Glu Gln Ile	50
40	
gag gca aat gac gat gtc gcg att ctc tct gag gaa gag gaa gtc gaa	367
Glu Ala Asn Asp Asp Val Ala Ile Leu Ser Glu Glu Glu Glu Val Glu	65
55	
att gaa ttg ctt cat gag ttt gaa acg att cct gtt tta tct gtt gag	415
Ile Glu Leu Leu His Glu Phe Glu Thr Ile Pro Val Leu Ser Val Glu	80
70	
tta agt cca gaa gat gtg gac gcg ctt gag ctc gat cca acg att tcg	463
Leu Ser Pro Glu Asp Val Asp Ala Leu Glu Leu Asp Pro Thr Ile Ser	100
85	
tat att gaa gag gat gca gaa gta acg aca atg gcg caa tca gtg cca	511
Tyr Ile Glu Glu Asp Ala Glu Val Thr Thr Met Ala Gln Ser Val Pro	115
105	
tgg gga att agc cgt gta caa gcc cca gct gcc cat aac cgt gga ttg	559
Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala His Asn Arg Gly Leu	130
120	
aca ggt tct ggt gta aaa gtt gct gtc ctc gat acg ggt att tcc acc	607
Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp Thr Gly Ile Ser Thr	145
135	
cat cca gac tta aat att cgc ggt ggt gct agc ttt gtg cca gga gaa	655
His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser Phe Val Pro Gly Glu	160
150	
cca tcc act caa gat gga aat gga cat ggc acg cat gtg gca ggg acg	703
Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr His Val Ala Gly Thr	180
165	
att gct gct tta aac aat tcg att ggc gtt ctg ggc gta gca ccg agc	751
Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly Val Ala Pro Ser	195
185	
gcg gaa cta tac gct gta aaa gta tta ggc gcg agc ggt tca ggt tcg	799
Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala Ser Gly Ser Gly Ser	210
200	
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SEQUENCE LISTING.txt

gtc agc tcg att gcc caa gga ttg gaa tgg gca ggg aac aat ggc atg Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala Gly Asn Asn Gly Met	847
215	
220	
225	
cac gtt gcg aat ttg agt tta gga agc ccg tcg ccg agt gca aca ctt His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser Pro Ser Ala Thr Leu	895
230	
235	
240	
gag caa gct gtt aat agc gct act tct aga ggc gtt ctt gtc gta gca Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly Val Leu Val Val Ala	943
245	
250	
255	
260	
gca tct ggt aat tca ggt gca ggc tca atc agc tat ccg gcc cgt tat Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser Tyr Pro Ala Arg Tyr	991
265	
270	
275	
gcg aac gca atg gca gtc gga gcg act gac caa aac aac aac cgc gct Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln Asn Asn Asn Arg Ala	1039
280	
285	
290	
agc ttt tca cag tat gga gct ggg ctt gac att gtc gcg cca ggt gtc Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile Val Ala Pro Gly Val	1087
295	
300	
305	
aat gtg cag agc aca tac cca ggt tca aca tat gcc agc tta aac ggt Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr Ala Ser Leu Asn Gly	1135
310	
315	
320	
aca tcg atg gct act cct cat gtt gca ggt gta gca gcc ctt gtt aaa Thr Ser Met Ala Thr Pro His Val Ala Gly Val Ala Ala Leu Val Lys	1183
325	
330	
335	
340	
caa aag aat cca tct tgg tcc aat gta caa atc cgc aat cat cta aag Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile Arg Asn His Leu Lys	1231
345	
350	
355	
aat acg gca acg ggt tta gga aac acg aac ttg tat gga agc ggg ctt Asn Thr Ala Thr Gly Leu Gly Asn Thr Asn Leu Tyr Gly Ser Gly Leu	1279
360	
365	
370	
gtc aat gca gaa gcg gca aca cgc taatcaataa taataacgct gtgtgcttta Val Asn Ala Glu Ala Ala Thr Arg	1333
375	
380	
agcacacagc gtttttttagt gtgtatgaat cgaaaaagag aaatagatcg ctgatttcaa aaagcgagcg taaagggcta ttgaagctct ttacgcttgc aggatttg	1393
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Glu Lys Tyr Leu Ile Gly Phe Asn Glu Gln Glu Ala Val Ser Glu Phe 35 40 45	

SEQUENCE LISTING.txt

Val Glu Gln Ile Glu Ala Asn Asp Asp Val Ala Ile Leu Ser Glu Glu
50 55 60

Glu Glu Val Glu Ile Glu Leu Leu His Glu Phe Glu Thr Ile Pro Val
65 70 75 80

Leu Ser Val Glu Leu Ser Pro Glu Asp Val Asp Ala Leu Glu Leu Asp
85 90 95

Pro Thr Ile Ser Tyr Ile Glu Glu Asp Ala Glu Val Thr Thr Met Ala
100 105 110

Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala His
115 120 125

Asn Arg Gly Leu Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp Thr
130 135 140

Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser Phe
145 150 155 160

Val Pro Gly Glu Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr His
165 170 175

Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly
180 185 190

Val Ala Pro Ser Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala Ser
195 200 205

Gly Ser Gly Ser Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala Gly
210 215 220

Asn Asn Gly Met His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser Pro
225 230 235 240

Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly Val
245 250 255

Leu Val Val Ala Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser Tyr
260 265 270

Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln Asn
275 280 285

Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile Val
290 295 300

Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr Ala
305 310 315 320

SEQUENCE LISTING.txt

Ser Leu Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Val Ala
325 330 335

Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile Arg
340 345 350

Asn His Leu Lys Asn Thr Ala Thr Gly Leu Gly Asn Thr Asn Leu Tyr
355 360 365

Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg
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<210> 22
<211> 46
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of the alkaline protease gene in *Bacillus clausii* KSM-K16 and its 5'-portion designed from nucleotide sequence of the upstream region of the alkaline cellulase gene in *Bacillus* sp. KSM-S237

<400> 22
actttaaaaa tatttaggag gtaatatgaa gaaaccgttg gggaaa 46

<210> 23
<211> 32
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide as PCR primer designed from nucleotide sequence of the downstream region of the alkaline protease gene in *Bacillus clausii* KSM-K16 with a insertion of the BglII restriction site at the 5'-end

<400> 23
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<210> 24
<211> 25
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide as PCR primer designed from nucleotide sequence of the upstream region of the alkaline cellulase gene in *Bacillus* sp. KSM-S237 with a insertion of the BamHI restriction site at the 5'-end

<400> 24
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<210> 25
<211> 46
<212> DNA
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SEQUENCE LISTING.txt

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 <223> Oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of the upstream region of the alkaline cellulase gene in Bacillus sp. KSM-S237 and its 5'-portion designed from nucleotide sequence of the alkaline protease gene in Bacillus clausii KSM-K16

<400> 25
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<210> 26
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> Oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of the alkaline amylase gene in Bacillus sp. KSM-K38 and its 5'-portion designed from nucleotide sequence of the alkaline cellulase gene in Bacillus sp. KSM-S237

<400> 26
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<210> 27
 <211> 30
 <212> DNA
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<220>
 <223> Oligonucleotide as PCR primer designed from nucleotide sequence of the downstream region of the alkaline amylase gene in Bacillus sp. KSM-K38 with a insertion of the XbaI restriction site at the 5'-end

<400> 27
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<210> 28
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <223> Oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of the alkaline cellulase gene in Bacillus sp. KSM-S237 and its 5'-portion designed from nucleotide sequence of the alkaline amylase gene in Bacillus sp. KSM-K38

<400> 28
 ttcaatccat ctgctgcaag agctgccgg 29